

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: RADIN, DAVID N.
CRAMER, CAROLE L.
OISHI, KAREN K.
WEISSENBORN, DEBORAH L.
- (ii) TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
PLANT-BASED EXPRESSION SYSTEMS
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Pennie & Edmonds
 - (B) STREET: 1155 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/003,737
 - (B) FILING DATE: 14-SEP-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Coruzzi, Laura A.
 - (B) REGISTRATION NUMBER: 30,742
 - (C) REFERENCE/DOCKET NUMBER: 7956-0011-999
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 790-9090
 - (B) TELEFAX: (212) 869-9741
 - (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGTCTAGAG TAAGCATCAT GGCTGGC

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CACGAATTCT GGCGACGCCA CAGGTAGGTG TGA

33

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGAGTTT CAAGTCCTTC CAGAGAGGAA TGTCCCAAGC CTTTGAGTAG GGTAAGCATC	60
ATGGCTGGCA GCCTCACAGG TTTGCTTCTA CTTCAGGCAG TGTCTGGGC ATCAGGTGCC	120
CGCCCTTGCA TCCCTAAAAG CTTCGGCTAC AGCTCGGTGG TGTGTGTCTG CAATGCCACA	180
TACTGTGACT CCTTGACCC CCCGACCTTT CCTGCCCTTG GTACCTTCAG CCGCTATGAG	240
AGTACACGCA GTGGGCGACG GATGGGCTG AGTATGGGC CCATCCAGGC TAATCACACG	300
GGCACAGGCC TGCTACTGAC CCTGCAGCCA GAACAGAAAGT TCCAGAAAGT GAAGGGATT	360
GGAGGGGCCA TGACAGATGC TGCTGCTCTC AACATCCTTG CCCTGTCACC CCCTGCCAA	420
AATTGCTAC TTAAATCGTA CTTCTCTGAA GAAGGAATCG GATATAACAT CATCCGGTA	480
CCCATGGCCA GCTGTGACTT CTCCATCCGC ACCTACACCT ATGCAGACAC CCCTGATGAT	540
TTCCAGTTGC ACAACTTCAG CCTCCCAGAG GAAGATACCA AGCTCAAGAT ACCCCTGATT	600
CACCGAGCCC TGCAGTTGGC CCAGCGTCCC GTTCACTCC TTGCCAGCCC CTGGACATCA	660
CCCACTTGGC TCAAGACCAA TGGAGCGGTG AATGGGAAGG GGTCACTCAA GGGACAGCCC	720
GGAGACATCT ACCACCAAGAC CTGGGCCAGA TACTTGTGA AGTCCCTGGA TGCCTATGCT	780
GAGCACAAGT TACAGTTCTG GGCAGTGACA GCTGAAAATG AGCCTTCTGC TGGGCTGTTG	840
AGTGGATACC CCTTCCAGTG CCTGGCTTC ACCCCTGAAC ATCAGCGAGA CTTCATTGCC	900
CGTGACCTAG GTCCTACCCCT CGCCAAACAGT ACTCACCAACA ATGTCCGCCT ACTCATGCTG	960
GATGACCAAC GCTTGCTGCT GCCCCACTGG GCAAAGGTGG TACTGACAGA CCCAGAAGCA	1020

GCTAAATATG TTCAATGGCAT TGCTGTACAT TGGTACCTGG ACTTTCTGGC TCCAGCCAAA	1080
GCCACCCCTAG GGGAGACACA CCGCCTGTTG CCCAACACCA TGCTCTTGC CTCAGAGGCC	1140
TGTGTGGGCT CCAAGTTCTG GGAGCAGAGT GTGCGGCTAG GCTCCTGGGA TCGAGGGATG	1200
CAGTACAGCC ACAGCATCAT CACGAACCTC CTGTACCATG TGGTCGGCTG GACCGACTGG	1260
AACCTTGCCC TGAACCCCGA AGGAGGACCC AATTGGGTGC GTAACTTTGT CGACAGTCCC	1320
ATCATTGTTAG ACGTCACCAAG GGACACGTTT TACAAACAGC CCATGTTCTA CCACCTTGGC	1380
CACTTCAGCA AGTTCATTCC TGAGGGCTCC CAGAGAGTGG GGCTGGTTGC CAGTCAGAAG	1440
AACGACCTGG ACGCAGTGGC ACTGATGCAT CCCGATGGCT CTGCTGTTGT GGTCGTGCTA	1500
AACCGCTCCT CTAAGGATGT GCCTCTTACC ATCAAGGATC CTGCTGTGGG CTTCTGGAG	1560
ACAATCTCAC CTGGCTACTC CATTGACACC TACCTGTGGC GTGCCAGAA TTCGGACTAC	1620
AAGGACGACG ATGACAAGTT GA	1642

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Glu	Phe	Ser	Ser	Pro	Ser	Arg	Glu	Glu	Cys	Pro	Lys	Pro	Leu	Ser
1					5				10					15	
Arg	Val	Ser	Ile	Met	Ala	Gly	Ser	Leu	Thr	Gly	Leu	Leu	Leu	Leu	Gln
					20				25					30	
Ala	Val	Ser	Trp	Ala	Ser	Gly	Ala	Arg	Pro	Cys	Ile	Pro	Lys	Ser	Phe
					35		40					45			
Gly	Tyr	Ser	Ser	Val	Val	Cys	Val	Cys	Asn	Ala	Thr	Tyr	Cys	Asp	Ser
					50		55				60				
Phe	Asp	Pro	Pro	Thr	Phe	Pro	Ala	Leu	Gly	Thr	Phe	Ser	Arg	Tyr	Glu
					65				75					80	
Ser	Thr	Arg	Ser	Gly	Arg	Arg	Met	Glu	Leu	Ser	Met	Gly	Pro	Ile	Gln
					85			90					95		
Ala	Asn	His	Thr	Gly	Thr	Gly	Leu	Leu	Leu	Thr	Leu	Gln	Pro	Glu	Gln
					100				105				110		
Lys	Phe	Gln	Lys	Val	Lys	Gly	Phe	Gly	Gly	Ala	Met	Thr	Asp	Ala	Ala
					115			120				125			
Ala	Leu	Asn	Ile	Leu	Ala	Ieu	Ser	Pro	Pro	Ala	Gln	Asn	Leu	Leu	
					130		135					140			
Lys	Ser	Tyr	Phe	Ser	Glu	Glu	Gly	Ile	Gly	Tyr	Asn	Ile	Ile	Arg	Val
					145		150				155				160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
 165 170 175
 Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
 180 185 190
 Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
 195 200 205
 Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
 210 215 220
 Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro
 225 230 235 240
 Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
 245 250 255
 Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu
 260 265 270
 Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu
 275 280 285
 Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly
 290 295 300
 Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu
 305 310 315 320
 Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
 325 330 335
 Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr
 340 345 350
 Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
 355 360 365
 Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser
 370 375 380
 Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
 385 390 395 400
 Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
 405 410 415
 Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
 420 425 430
 Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Val Thr Lys Asp
 435 440 445
 Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 450 455 460
 Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys
 465 470 475 480
 Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
 485 490 495
 Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys
 500 505 510
 Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile

515	520	525
His Thr Tyr Leu Trp Arg Arg	Gln Asn Ser Asp Tyr	Lys Asp Asp Asp
530	535	540
Asp Lys		
545		

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "MeGA Promoter"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CAATACGATA TTACCGAATA TTATACTAAA TCAAAATTAA ATTTATCATA TCAATTATTA	60
AACTGATATT TCAAATTAA ATATTTAATA TCTACTTCA ACTATTATTA CCTAATTATC	120
AAATGCAAAA TGTATGAGTT ATTCATAAT AGCCCAGTTC GTATCCAAAT ATTTTACACT	180
TGACCAGTCA ACTTGACTAT ATAAAACTTT ACTTCAAAAA ATTAAAAAAA AAAGAAAGTA	240
TATTATTGTA AAAGATAATA CTCCATTCAA AATATAAAAT GAAAAAAGTC CAGCGCGGCA	300
ACCGGGTTCC TATAAATACA TTTCCTACAT CTTCTCTTCT CCTCACATCC CATCACTCTT	360
CTTTAACAA TTATACTTGT CAATCATCAA TCCCACAAAC AACACTTTT CTCTCCTCTT	420
TTTCCTCACC GGCGGCAGAC TTACCGGTGA AAGTAAGCAG STC	463

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTAGTCTAGA ATGCGTCCCC TGCGCCCCCG CG	32
-------------------------------------	----

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGAATTCGAG CTCTCATGGA TTGCCCGGGG ATG

33

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2067 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGCGTCCCC	TGCGCCCCCG	CGCCGCGCTG	CTGGCGCTCC	TGGCCTCGCT	CCTGGCCGCG	60
CCCCCGGTGG	CCCCGGCCGA	GGCCCCGCAC	CTGGTGCAGG	TGGACGCGGC	CCGCGCGCTG	120
TGGCCCCCTGC	GGCGCTTCTG	GAGGAGCACA	GGCTTCTGCC	CCCCGCTGCC	ACACAGCCAG	180
GCTGACCAGT	ACGTCCCTCAG	CTGGGACCAAG	CAGCTCAACC	TCGCCTATGT	GGGCGCCGTC	240
CCTCACCGCG	GCATCAAGCA	GGTCCGGACC	CACTGGCTGC	TGGAGCTTGT	CACCACCAGG	300
GGGTCCACTG	GACGGGGCCT	GAGCTACAAC	TTCACCCACC	TGGACGGGTA	CTTGGACCTT	360
CTCAGGGAGA	ACCAGCTCCT	CCCAGGGTTT	GAGCTGATGG	GCAGGCCCTC	GGGCCACTTC	420
ACTGACTTTG	AGGACAAGCA	GCAGGTGTTT	GAGTGGAGG	ACTTGGTCTC	CAGCCTGGCC	480
AGGAGATACA	TCGGTAGGTA	CGGACTGGCG	CATGTTCCA	AGTGGAACTT	CGAGACGTGG	540
AATGAGCCAG	ACCACCAACGA	CTTGACAAC	GTCTCCATGA	CCATGCAAGG	CTTCCTGAAC	600
TACTACGATG	CCTGCTCGGA	GGGTCTGCGC	GCCGCCAGCC	CCGCCCTGCG	GCTGGGAGGC	660
CCCGGCGACT	CCTTCCACAC	CCCACCGCGA	TCCCCGCTGA	GCTGGGGCCT	CCTGCGCCAC	720
TGCCACGACG	GTACCAACTT	CTTCACTGGG	GAGGCGGGCG	TGCGGCTGGA	CTACATCTCC	780
CTCCACAGGA	AGGGTGCAGC	CAGCTCCATC	TCCATCCTGG	AGCAGGAGAA	GGTCGTGCG	840
CACGAGATCC	GGCAGCTCTT	CCCCAAGTTC	GCGGACACCC	CCATTACAA	CGACGAGGCG	900
GACCCGCTGG	TGGGCTGGTC	CCTGCCACAG	CCGTGGAGGG	CGGACGTGAC	CTACGCGGCC	960
ATGGTGGTGA	AGGTCACTCGC	GCAGCATCAG	AACCTGCTAC	TGGCCAACAC	CACCTCCGCC	1020
TTCCCCCTACG	CGCTCCTGAG	CAACGACAAT	GCCTTCCCTGA	GCTACCACCC	GCACCCCTTC	1080
GCGCAGCGCA	CGCTCACCGC	GCGCTTCCAG	GTCAACAACA	CCCGCCCGCC	GCACGTGCG	1140
CTGTTGCGCA	AGCCGGTGCT	CACGGCCATG	GGGCTGCTGG	CGCTGCTGGA	TGAGGAGCAG	1200
CTCTGGGCCG	AAGTGTGCGA	GGCCGGGACC	GTCCTGGACA	GCAACCACAC	GGTGGCGTC	1260
CTGGCCAGCG	CCCACCGGCC	CCAGGGCCCG	GCCGACGCCT	GGCGCGCCGC	GGTGCTGATC	1320

TACGCGAGCG	ACGACACCCG	CGCCCACCCC	AACCGCAGCG	TCGCGGTGAC	CCTGCGGCTG	1380
CGCGGGGTGC	CCCCCGGCC	GGGCCTGGTC	TACGTCACGC	GCTACCTGGA	CAACGGGCTC	1440
TGCAGCCCCG	ACGGCGAGTG	CGGGCGCCTG	GGCCGGCCCG	TCTTCCCCAC	GGCAGAGCAG	1500
TTCCGGCGCA	TGCGCGCGGC	TGAGGACCCG	GTGGCCGCGG	CGCCCCGCC	CTTACCCGCC	1560
GGCGGCCGCC	TGACCCCTGCG	CCCCGCGCTG	CGGCTGCCGT	CGCTTTGCT	GGTGCACGTG	1620
TGTGCGCGCC	CCGAGAAAGCC	GCCCCGGCAG	GTCACGCGGC	TCCGCGCCCT	GCCCCTGACC	1680
CAAGGGCAGC	TGGTTCTGGT	CTGGTCGGAT	GAACACGTGG	GCTCCAAGTG	CCTGTGGACA	1740
TACGAGATCC	AGTTCTCTCA	GGACGGTAAG	GCGTACACCC	CGGTCAGCAG	GAAGCCATCG	1800
ACCTTCAACC	TCTTGTGTT	CAGCCCAGAC	ACAGGTGCTG	TCTCTGGCTC	CTACCGAGTT	1860
CGAGCCCTGG	ACTACTGGC	CCGACCAGGC	CCCTTCTCGG	ACCCTGTGCC	GTACCTGGAG	1920
GTCCCTGTGC	CAAGAGGGCC	CCCATCCCCG	GGCAATCCAT	GAGCCTGTGC	TGAGCCCCAG	1980
TGGGTTGCAC	CTCCACCGGC	AGTCAGCGAG	CTGGGGCTGC	ACTGTGCCCA	TGCTGCCCTC	2040
CCATCACCCC	CTTGCAATA	TATTTTT				2067

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Arg	Pro	Leu	Arg	Pro	Arg	Ala	Ala	Leu	Leu	Ala	Leu	Leu	Ala	Ser
1					5					10					15
Leu	Leu	Ala	Ala	Pro	Pro	Val	Ala	Pro	Ala	Glu	Ala	Pro	His	Leu	Val
					20				25			30			
His	Val	Asp	Ala	Ala	Arg	Ala	Leu	Trp	Pro	Leu	Arg	Arg	Phe	Trp	Arg
					35			40			45				
Ser	Thr	Gly	Phe	Cys	Pro	Pro	Leu	Pro	His	Ser	Gln	Ala	Asp	Gln	Tyr
					50			55			60				
Val	Leu	Ser	Trp	Asp	Gln	Gln	Leu	Asn	Leu	Ala	Tyr	Val	Gly	Ala	Val
	65				70				75			80			
Pro	His	Arg	Gly	Ile	Lys	Gln	Val	Arg	Thr	His	Trp	Leu	Leu	Glu	Leu
					85			90			95				
Val	Thr	Thr	Arg	Gly	Ser	Thr	Gly	Arg	Gly	Leu	Ser	Tyr	Asn	Phe	Thr
	100							105				110			
His	Leu	Asp	Gly	Thr	Leu	Asp	Leu	Leu	Arg	Glu	Asn	Gln	Leu	Leu	Pro
	115						120				125				
Gly	Phe	Glu	Leu	Met	Gly	Ser	Ala	Ser	Gly	His	Phe	Thr	Asp	Phe	Glu
	130				135					140					

Asp Lys Gln Gln Val Phe	Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
145	150
Arg Arg Tyr Ile Gly Arg	Tyr Gly Leu Ala His Val Ser Lys Trp Asn
165	170
Phe Glu Thr Trp Asn Glu	Pro Asp His His Asp Phe Asp Asn Val Ser
180	185
Met Thr Met Gln Gly Phe	Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
195	200
Leu Arg Ala Ala Ser Pro	Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
210	215
Phe His Thr Pro Pro Arg	Ser Pro Leu Ser Trp Gly Leu Leu Arg His
225	230
Cys His Asp Gly Thr Asn	Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
245	250
Asp Tyr Ile Ser Leu His	Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
260	265
Leu Glu Gln Glu Lys Val	Val Ala Gln Glu Ile Arg Gln Leu Phe Pro
275	280
Lys Phe Ala Asp Thr Pro	Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val
290	295
Gly Trp Ser Leu Pro Gln	Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
305	310
Met Val Val Lys Val Ile	Ala Gln His Gln Asn Leu Leu Leu Ala Asn
325	330
Thr Thr Ser Ala Phe Pro	Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe
340	345
Leu Ser Tyr His Pro His	Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg
355	360
Phe Gln Val Asn Asn Thr	Arg Pro Pro His Val Gln Leu Leu Arg Lys
370	375
Pro Val Leu Thr Ala Met	Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
385	390
Leu Trp Ala Glu Val Ser	Gln Ala Gly Thr Val Leu Asp Ser Asn His
405	410
Thr Val Gly Val Leu Ala	Ser Ala His Arg Pro Gln Gly Pro Ala Asp
420	425
Ala Trp Arg Ala Ala Val	Ile Tyr Ala Ser Asp Asp Thr Arg Ala
435	440
His Pro Asn Arg Ser Val	Ala Val Thr Leu Arg Leu Arg Gly Val Pro
450	455
Pro Gly Pro Gly Leu Val	Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
465	470
Cys Ser Pro Asp Gly Glu	Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
485	490
Thr Ala Glu Gln Phe Arg	Arg Met Arg Ala Ala Glu Asp Pro Val Ala

500	505	510	
Ala Ala Pro Arg Pro Leu Pro	Ala Gly Gly Arg Leu Thr	Leu Arg Pro	
515	520	525	
Ala Leu Arg Leu Pro Ser	Leu Leu Leu Val His Val Cys Ala Arg Pro		
530	535	540	
Glu Lys Pro Pro Gly	Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr		
545	550	555	560
Gln Gly Gln Leu Val	Leu Val Trp Ser Asp Glu His Val Gly Ser Lys		
565	570	575	
Cys Leu Trp Thr Tyr	Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr		
580	585	590	
Thr Pro Val Ser Arg	Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser		
595	600	605	
Pro Asp Thr Gly Ala Val	Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp		
610	615	620	
Tyr Trp Ala Arg Pro	Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu		
625	630	635	640
Val Pro Val Pro Arg	Gly Pro Pro Ser Pro Gly Asn Pro		
645	650		

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asp Tyr Lys Asp Asp Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCTATGCTG AGCACAAAGTT ACAG

24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Complementary sequence of a
PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCCCTTGAGC TCGTCACTGG CGACGCCACA GGTA

34